(FILE 'HOME' ENTERED AT 15:14:05 ON 21 JUN 2002)

FILE 'BIOSIS, MEDLINE, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 15:14:31 ON 21 JUN 2002

L1	1584	S	ANAPHASE PROMOTING COMPLEX
L2	34042	S	UBIQUITIN
L3	785	S	L1 AND L2
L4	137783	S	RECOMBINANT PROTEIN
L5	12	S	L3 AND L4
L6	8		DUPLICATE REMOVE L5 (4 DUPLICATES REMOVED)

L6 ANSWER 7 OF 8 MEDLINE
AN 96217916 MEDLINE
DN 96217916 PubMed ID: 8632802
TI Cut2 proteolysis required for sister-chromatid seperation in fission yeast.
AU Funabiki H; Yamano H; Kumada K; Nagao K; Hunt T; Yanagida M
CS Department of Biophysics, Faculty of Science, Kyoto University, Japan.
SO NATURE, (1996 May 30) 381 (6581) 438-41.
Journal code: 0410462. ISSN: 0028-0836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199607
ED Entered STN: 19960715
Last Updated on STN: 19960715
Entered Medline: 19960703
AB Although mitotic cyclins are well-known substrates for **ubiquitin**-mediated proteolysis at the metaphase-anaphase transition, their degradation is not essential for separation of sister chromatids; several lines of evidence suggest that proteolysis of other protein(s) is required, however. Here we report the anaphase-specific proteolysis of the Schizosaccharomyces pombe Cut2 protein, which is essential for sister-chromatid separation. Cut2 is located in the nucleus, where it is concentrated along the short metaphase spindle. The rapid degradation of Cut2 at anaphase requires its amino-terminal region and the activity of Cut9 (ref. 14), a component of the 20S cyclosome/**anaphase-promoting complex** (APC), which is necessary for cyclin destruction. Expression of non-degradable Cut2 blocks sister-chromatid separation but not cell-cycle progression. This defect can be overcome by grafting the N terminus of cyclin B onto the truncated Cut2, demonstrating that the regulated proteolysis of Cut2 is essential for sister-chromatid separation.
CT Check Tags: Support, Non-U.S. Gov't
Amino Acid Sequence
Cell Division: PH, physiology
Cell Nucleus: PH, physiology
*Chromatids
*Fungal Proteins: ME, metabolism
Molecular Sequence Data
Recombinant Proteins: ME, metabolism
Schizosaccharomyces: CY, cytology
*Schizosaccharomyces: GE, genetics
Schizosaccharomyces: ME, metabolism
CN 0 (Fungal Proteins); 0 (**Recombinant Proteins**)

L6 ANSWER 8 OF 8 MEDLINE
AN 95254637 MEDLINE
DN 95254637 PubMed ID: 7736580
TI A 20S complex containing CDC27 and CDC16 catalyzes the mitosis-specific conjugation of **ubiquitin** to cyclin B.
AU King R W; Peters J M; Tugendreich S; Rolfe M; Hieter P; Kirschner M W
CS Department of Cell Biology, Harvard Medical School, Boston, Massachusetts 02115, USA.
NC GM26875-17 (NIGMS)
GM39023-08 (NIGMS)
SO CELL, (1995 Apr 21) 81 (2) 279-88.
Journal code: 0413066. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199506
ED Entered STN: 19950615

Last Updated on STN: 19950615
Entered Medline: 19950602

AB Cyclin B is degraded at the onset of anaphase by a **ubiquitin**-dependent proteolytic system. We have fractionated mitotic Xenopus egg extracts to identify components required for this process. We find that UBC4 and at least one other **ubiquitin**-conjugating enzyme can support cyclin B ubiquitination. The mitotic specificity of cyclin ubiquitination is determined by a 20S complex that contains homologs of budding yeast CDC16 and CDC27. Because these proteins are required for anaphase in yeast and mammalian cells, we refer to this complex as the **anaphase-promoting complex** (APC). CDC27 antibodies deplete APC activity, while immunopurified CDC27 complexes are sufficient to complement either interphase extracts or a mixture of recombinant UBC4 and the **ubiquitin**-activating enzyme E1. These results suggest that APC functions as a regulated **ubiquitin**-protein ligase that targets cyclin B for destruction in mitosis.

CT Check Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Anaphase: PH, physiology
*Cell Cycle Proteins: ME, metabolism
*Cyclins: ME, metabolism
Ligases: AN, analysis
Ligases: GE, genetics
Ligases: ME, metabolism
Macromolecular Systems
*Mitosis: PH, physiology
Ovum
Recombinant Proteins: PD, pharmacology
Subcellular Fractions: ME, metabolism
***Ubiquitins: ME, metabolism**
Xenopus

RN 147015-50-7 (cdc27 protein)

CN 0 (Cdc16 protein); 0 (Cell Cycle Proteins); 0 (Cyclins); 0 (Macromolecular Systems); 0 (**Recombinant Proteins**); 0 (**Ubiquitins**); EC 6. (Ligases); EC 6.3.2.- (**ubiquitin**-conjugating enzyme E2); EC 6.3.2.- (**ubiquitin**-conjugating enzyme UBC4); EC 6.3.2.19 (**ubiquitin**-protein ligase)